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RAW SEQUENCE LISTING

DATE: 08/05/2004

PATENT APPLICATION: US/10/735,972

TIME: 12:31:21

Input Set : A:\07917-198001.TXT

Output Set: N:\CRF4\08052004\J735972.raw

4 <110> APPLICANT: Pereira, Andrea
 5 Wentworth, Diana Bilodeau
 6 Gandhi, Rita
 8 <120> TITLE OF INVENTION: KINESIN-LIKE PROTEINS AND METHODS OF USE
 11 <130> FILE REFERENCE: 07917-198001
 13 <140> CURRENT APPLICATION NUMBER: US 10/735,972
 14 <141> CURRENT FILING DATE: 2003-12-15
 16 <150> PRIOR APPLICATION NUMBER: US 60/433,098
 17 <151> PRIOR FILING DATE: 2002-12-13
 19 <160> NUMBER OF SEQ ID NOS: 16
 21 <170> SOFTWARE: FastSEQ for Windows Version 4.0

23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 2697
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (1)...(2694)
 32 <400> SEQUENCE: 1

33 atg tct gtc act gag gaa gac ctg tgc cac cat atg aaa gta gta gtt 48
 34 Met Ser Val Thr Glu Glu Asp Leu Cys His His Met Lys Val Val Val
 35 1 5 10 15
 37 cgt gta cgt ccg gaa aac act aaa gaa aaa gca gct gga ttt cat aaa 96
 38 Arg Val Arg Pro Glu Asn Thr Lys Glu Lys Ala Ala Gly Phe His Lys
 39 20 25 30
 41 gtg gtt cat gtt gtg gat aaa cat atc cta gtt ttt gat ccc aaa caa 144
 42 Val Val His Val Val Asp Lys His Ile Leu Val Phe Asp Pro Lys Gln
 43 35 40 45
 45 gaa gaa gtc agt ttt ttc cat gga aag aaa act aca aat caa aat gtt 192
 46 Glu Glu Val Ser Phe Phe His Gly Lys Lys Thr Thr Asn Gln Asn Val
 47 50 55 60
 49 ata aag aaa caa aat aag gat ctt aaa ttt gta ttt gat gct gtt ttt 240
 50 Ile Lys Lys Gln Asn Lys Asp Leu Lys Phe Val Phe Asp Ala Val Phe
 51 65 70 75 80
 53 gat gaa acg tca act cag tca gaa gtt ttt gaa cac act act aag cca 288
 54 Asp Glu Thr Ser Thr Gln Ser Glu Val Phe Glu His Thr Thr Lys Pro
 55 85 90 95
 57 att ctt cgt agt ttt ttg aat gga tat aat tgc aca gta ctt gcc tat 336
 58 Ile Leu Arg Ser Phe Leu Asn Gly Tyr Asn Cys Thr Val Leu Ala Tyr
 59 100 105 110
 61 ggt gcc act ggt gct ggg aag acc cac act atg cta gga tca gct gat 384
 62 Gly Ala Thr Gly Ala Gly Lys Thr His Thr Met Leu Gly Ser Ala Asp
 63 115 120 125

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65 gaa cct gga gtg atg tat cta aca atg tta cac ctt tac aaa tgc atg      432
66 Glu Pro Gly Val Met Tyr Leu Thr Met Leu His Leu Tyr Lys Cys Met
67      130                      135                      140
69 gat gag att aaa gaa gag aaa ata tgt agt act gca gtt tca tat ctg      480
70 Asp Glu Ile Lys Glu Glu Lys Ile Cys Ser Thr Ala Val Ser Tyr Leu
71 145                      150                      155                      160
73 gag gta tat aat gaa cag att cgt gat ctc tta gta aat tca ggg cca      528
74 Glu Val Tyr Asn Glu Gln Ile Arg Asp Leu Leu Val Asn Ser Gly Pro
75      165                      170                      175
77 ctt gct gtc cgg gaa gat acc caa aaa ggg gtg gtc gtt cat gga ctt      576
78 Leu Ala Val Arg Glu Asp Thr Gln Lys Gly Val Val Val His Gly Leu
79      180                      185                      190
81 act tta cac cag ccc aaa tcc tca gaa gaa att tta cat tta ttg gat      624
82 Thr Leu His Gln Pro Lys Ser Ser Glu Glu Ile Leu His Leu Leu Asp
83      195                      200                      205
85 aat gga aac aaa aac agg aca caa cat ccc act gat atg aat gcc aca      672
86 Asn Gly Asn Lys Asn Arg Thr Gln His Pro Thr Asp Met Asn Ala Thr
87      210                      215                      220
89 tct tct cgt tct cat gct gtt ttc caa att tac ttg cga caa caa gac      720
90 Ser Ser Arg Ser His Ala Val Phe Gln Ile Tyr Leu Arg Gln Gln Asp
91 225                      230                      235                      240
93 aaa aca gca agt atc aat caa aat gtc cgt att gcc aag atg tca ctc      768
94 Lys Thr Ala Ser Ile Asn Gln Asn Val Arg Ile Ala Lys Met Ser Leu
95      245                      250                      255
97 att gac ctg gca gga tct gag cga gca agt act tcc ggt gct aag ggg      816
98 Ile Asp Leu Ala Gly Ser Glu Arg Ala Ser Thr Ser Gly Ala Lys Gly
99      260                      265                      270
101 acc cga ttt gta gaa ggc aca aat att aat aga tca ctt tta gct ctt      864
102 Thr Arg Phe Val Glu Gly Thr Asn Ile Asn Arg Ser Leu Leu Ala Leu
103      275                      280                      285
105 ggg aat gtc atc aat gcc tta gca gat tca aag aga aag aat cag cat      912
106 Gly Asn Val Ile Asn Ala Leu Ala Asp Ser Lys Arg Lys Asn Gln His
107      290                      295                      300
109 atc cct tac aga aat agt aag ctt act cgc ttg tta aag gat tct ctt      960
110 Ile Pro Tyr Arg Asn Ser Lys Leu Thr Arg Leu Leu Lys Asp Ser Leu
111 305                      310                      315                      320
113 gga gga aac tgt caa act ata atg ata gct gct gtt agt cct tcc tct      1008
114 Gly Gly Asn Cys Gln Thr Ile Met Ile Ala Ala Val Ser Pro Ser Ser
115      325                      330                      335
117 gta ttc tac gat gac aca tat aac act ctt aag tat gct aac cgg gca      1056
118 Val Phe Tyr Asp Asp Thr Tyr Asn Thr Leu Lys Tyr Ala Asn Arg Ala
119      340                      345                      350
121 aag gac att aaa tct tct ttg aag agc aat gtt ctt aat gtc aat aat      1104
122 Lys Asp Ile Lys Ser Ser Leu Lys Ser Asn Val Leu Asn Val Asn Asn
123      355                      360                      365
125 cat ata act caa tat gta aag atc tgt aat gag cag aag gca gag att      1152
126 His Ile Thr Gln Tyr Val Lys Ile Cys Asn Glu Gln Lys Ala Glu Ile
127      370                      375                      380
129 tta ttg tta aaa gaa aaa cta aaa gcc tat gaa gaa cag aaa gcc ttc      1200

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130	Leu	Leu	Leu	Lys	Glu	Lys	Leu	Lys	Ala	Tyr	Glu	Glu	Gln	Lys	Ala	Phe	
131	385					390					395					400	
133	act	aat	gaa	aat	gac	caa	gca	aag	tta	atg	att	tca	aac	cct	cag	gaa	1248
134	Thr	Asn	Glu	Asn	Asp	Gln	Ala	Lys	Leu	Met	Ile	Ser	Asn	Pro	Gln	Glu	
135					405					410					415		
137	aaa	gaa	atc	gaa	agg	ttt	caa	gaa	atc	ctg	aac	tgc	ttg	ttc	cag	aat	1296
138	Lys	Glu	Ile	Glu	Arg	Phe	Gln	Glu	Ile	Leu	Asn	Cys	Leu	Phe	Gln	Asn	
139				420					425					430			
141	cga	gaa	gaa	att	aga	caa	gaa	tat	ctg	aag	ttg	gaa	atg	tta	ctt	aaa	1344
142	Arg	Glu	Glu	Ile	Arg	Gln	Glu	Tyr	Leu	Lys	Leu	Glu	Met	Leu	Leu	Lys	
143				435					440					445			
145	gaa	aat	gaa	ctt	aaa	tca	ttc	tac	caa	caa	cag	tgc	cat	aaa	caa	ata	1392
146	Glu	Asn	Glu	Leu	Lys	Ser	Phe	Tyr	Gln	Gln	Gln	Cys	His	Lys	Gln	Ile	
147		450					455					460					
149	gaa	atg	atg	tgt	tct	gaa	gac	aaa	gta	gaa	aag	gcc	act	gga	aaa	cga	1440
150	Glu	Met	Met	Cys	Ser	Glu	Asp	Lys	Val	Glu	Lys	Ala	Thr	Gly	Lys	Arg	
151	465					470					475				480		
153	gat	cat	aga	ctt	gca	atg	ttg	aaa	act	cgt	cgc	tcc	tac	ctg	gag	aaa	1488
154	Asp	His	Arg	Leu	Ala	Met	Leu	Lys	Thr	Arg	Arg	Ser	Tyr	Leu	Glu	Lys	
155				485						490					495		
157	agg	agg	gag	gag	gaa	ttg	aag	caa	ttt	gat	gag	aat	act	aat	tgg	ctc	1536
158	Arg	Arg	Glu	Glu	Glu	Leu	Lys	Gln	Phe	Asp	Glu	Asn	Thr	Asn	Trp	Leu	
159				500					505					510			
161	cat	cgt	gtc	gaa	aaa	gaa	atg	gga	ctc	tta	agt	caa	aac	ggt	cat	att	1584
162	His	Arg	Val	Glu	Lys	Glu	Met	Gly	Leu	Leu	Ser	Gln	Asn	Gly	His	Ile	
163				515					520					525			
165	cca	aag	gaa	ctc	aag	aaa	gat	ctt	cat	tgt	cac	cat	ttg	cac	ctc	cag	1632
166	Pro	Lys	Glu	Leu	Lys	Lys	Asp	Leu	His	Cys	His	His	Leu	His	Leu	Gln	
167		530					535					540					
169	aac	aaa	gat	ttg	aaa	gca	caa	att	aga	cat	atg	atg	gat	cta	gct	tgt	1680
170	Asn	Lys	Asp	Leu	Lys	Ala	Gln	Ile	Arg	His	Met	Met	Asp	Leu	Ala	Cys	
171	545					550					555				560		
173	ctt	cag	gaa	cag	caa	cac	agg	cag	act	gaa	gca	gta	ttg	aat	gct	tta	1728
174	Leu	Gln	Glu	Gln	Gln	His	Arg	Gln	Thr	Glu	Ala	Val	Leu	Asn	Ala	Leu	
175				565						570					575		
177	ctt	cca	acc	cta	aga	aaa	caa	tat	tgc	aca	tta	aaa	gaa	gcc	ggc	ctg	1776
178	Leu	Pro	Thr	Leu	Arg	Lys	Gln	Tyr	Cys	Thr	Leu	Lys	Glu	Ala	Gly	Leu	
179				580					585					590			
181	tca	aat	gct	gct	ttt	gaa	tct	gac	ttc	aaa	gag	atc	gaa	cat	ttg	gta	1824
182	Ser	Asn	Ala	Ala	Phe	Glu	Ser	Asp	Phe	Lys	Glu	Ile	Glu	His	Leu	Val	
183				595					600					605			
185	gag	agg	aaa	aaa	gtg	gta	gtt	tgg	gct	gac	caa	act	gcc	gaa	caa	cca	1872
186	Glu	Arg	Lys	Lys	Val	Val	Val	Trp	Ala	Asp	Gln	Thr	Ala	Glu	Gln	Pro	
187		610					615					620					
189	aag	caa	aac	gat	cta	cca	ggg	att	tct	ggt	ctt	atg	acc	ttt	cca	caa	1920
190	Lys	Gln	Asn	Asp	Leu	Pro	Gly	Ile	Ser	Val	Leu	Met	Thr	Phe	Pro	Gln	
191	625					630					635				640		
193	ctt	gga	cca	gtt	cag	cct	att	cct	tgt	tgc	tca	tct	tca	ggt	gga	act	1968
194	Leu	Gly	Pro	Val	Gln	Pro	Ile	Pro	Cys	Cys	Ser	Ser	Ser	Gly	Gly	Thr	

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195          645          650          655
197 aat ctg gtt aag att cct aca gaa aaa aga act cgg aga aaa cta atg      2016
198 Asn Leu Val Lys Ile Pro Thr Glu Lys Arg Thr Arg Arg Lys Leu Met
199          660          665          670
201 cca tct ccc ttg aaa gga cag cat act cta aag tct cca cca tct caa      2064
202 Pro Ser Pro Leu Lys Gly Gln His Thr Leu Lys Ser Pro Pro Ser Gln
203          675          680          685
205 agt gtg cag ctc aat gat tct ctt agc aaa gaa ctt cag cct att gta      2112
206 Ser Val Gln Leu Asn Asp Ser Leu Ser Lys Glu Leu Gln Pro Ile Val
207          690          695          700
209 tat aca cca gaa gac tgt aga aaa gct ttt caa aat ccg tct aca gta      2160
210 Tyr Thr Pro Glu Asp Cys Arg Lys Ala Phe Gln Asn Pro Ser Thr Val
211 705          710          715          720
213 acc tta atg aaa cca tca tca ttt act aca agt ttt cag gct atc agc      2208
214 Thr Leu Met Lys Pro Ser Ser Phe Thr Thr Ser Phe Gln Ala Ile Ser
215          725          730          735
217 tca aac ata aac agt gat aat tgt ctg aaa atg ttg tgt gaa gta gct      2256
218 Ser Asn Ile Asn Ser Asp Asn Cys Leu Lys Met Leu Cys Glu Val Ala
219          740          745          750
221 atc cct cat aat aga aga aaa gaa tgt gga cag gag gac ttg gac tct      2304
222 Ile Pro His Asn Arg Arg Lys Glu Cys Gly Gln Glu Asp Leu Asp Ser
223          755          760          765
225 aca ttt act ata tgt gaa gac atc aag agc tcg aag tgt aaa tta ccc      2352
226 Thr Phe Thr Ile Cys Glu Asp Ile Lys Ser Ser Lys Cys Lys Leu Pro
227          770          775          780
229 gaa caa gaa tca cta cca aat gat aac aaa gac att tta caa cgg ctt      2400
230 Glu Gln Glu Ser Leu Pro Asn Asp Asn Lys Asp Ile Leu Gln Arg Leu
231 785          790          795          800
233 gat cct tct tca ttc tca act aag cat tct atg cct gta cca agc atg      2448
234 Asp Pro Ser Ser Phe Ser Thr Lys His Ser Met Pro Val Pro Ser Met
235          805          810          815
237 gtg cca tcc tac atg gca atg act act gct gcc aaa agg aaa cgg aaa      2496
238 Val Pro Ser Tyr Met Ala Met Thr Thr Ala Ala Lys Arg Lys Arg Lys
239          820          825          830
241 tta aca agt tct aca tca aac agt tcg tta act gca gac gta aat tct      2544
242 Leu Thr Ser Ser Thr Ser Asn Ser Ser Leu Thr Ala Asp Val Asn Ser
243          835          840          845
245 gga ttt gcc aaa cgt gtt cga caa gat aat tca agt gag aag cac tta      2592
246 Gly Phe Ala Lys Arg Val Arg Gln Asp Asn Ser Ser Glu Lys His Leu
247          850          855          860
249 caa gaa aac aaa cca aca atg gaa cat aaa aga aac atc tgt aaa ata      2640
250 Gln Glu Asn Lys Pro Thr Met Glu His Lys Arg Asn Ile Cys Lys Ile
251 865          870          875          880
253 aat cca agc atg gtt aga aaa ttt gga aga aat att tca aaa gga aat      2688
254 Asn Pro Ser Met Val Arg Lys Phe Gly Arg Asn Ile Ser Lys Gly Asn
255          885          890          895
257 cta aga taa      2697
258 Leu Arg
262 <210> SEQ ID NO: 2

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263 <211> LENGTH: 898

264 <212> TYPE: PRT

265 <213> ORGANISM: Homo sapiens

267 <400> SEQUENCE: 2

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271           20           25           30
272 Val Val His Val Val Asp Lys His Ile Leu Val Phe Asp Pro Lys Gln
273           35           40           45
274 Glu Glu Val Ser Phe Phe His Gly Lys Lys Thr Thr Asn Gln Asn Val
275           50           55           60
276 Ile Lys Lys Gln Asn Lys Asp Leu Lys Phe Val Phe Asp Ala Val Phe
277 65           70           75           80
278 Asp Glu Thr Ser Thr Gln Ser Glu Val Phe Glu His Thr Thr Lys Pro
279           85           90           95
280 Ile Leu Arg Ser Phe Leu Asn Gly Tyr Asn Cys Thr Val Leu Ala Tyr
281           100          105          110
282 Gly Ala Thr Gly Ala Gly Lys Thr His Thr Met Leu Gly Ser Ala Asp
283           115          120          125
284 Glu Pro Gly Val Met Tyr Leu Thr Met Leu His Leu Tyr Lys Cys Met
285           130          135          140
286 Asp Glu Ile Lys Glu Glu Lys Ile Cys Ser Thr Ala Val Ser Tyr Leu
287 145          150          155          160
288 Glu Val Tyr Asn Glu Gln Ile Arg Asp Leu Leu Val Asn Ser Gly Pro
289           165          170          175
290 Leu Ala Val Arg Glu Asp Thr Gln Lys Gly Val Val Val His Gly Leu
291           180          185          190
292 Thr Leu His Gln Pro Lys Ser Ser Glu Glu Ile Leu His Leu Leu Asp
293           195          200          205
294 Asn Gly Asn Lys Asn Arg Thr Gln His Pro Thr Asp Met Asn Ala Thr
295           210          215          220
296 Ser Ser Arg Ser His Ala Val Phe Gln Ile Tyr Leu Arg Gln Gln Asp
297 225          230          235          240
298 Lys Thr Ala Ser Ile Asn Gln Asn Val Arg Ile Ala Lys Met Ser Leu
299           245          250          255
300 Ile Asp Leu Ala Gly Ser Glu Arg Ala Ser Thr Ser Gly Ala Lys Gly
301           260          265          270
302 Thr Arg Phe Val Glu Gly Thr Asn Ile Asn Arg Ser Leu Leu Ala Leu
303           275          280          285
304 Gly Asn Val Ile Asn Ala Leu Ala Asp Ser Lys Arg Lys Asn Gln His
305           290          295          300
306 Ile Pro Tyr Arg Asn Ser Lys Leu Thr Arg Leu Leu Lys Asp Ser Leu
307 305          310          315          320
308 Gly Gly Asn Cys Gln Thr Ile Met Ile Ala Ala Val Ser Pro Ser Ser
309           325          330          335
310 Val Phe Tyr Asp Asp Thr Tyr Asn Thr Leu Lys Tyr Ala Asn Arg Ala
311           340          345          350
312 Lys Asp Ile Lys Ser Ser Leu Lys Ser Asn Val Leu Asn Val Asn Asn

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VERIFICATION SUMMARY

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